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Result
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Perfect score:
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Maximum DB seq length: 200000000
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Post-processing: Minimum Match 0%
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Scoring table:
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                                                                                                                                                                                                                                                                                                                                                                                       Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.
                    2516.5
2386.5
2385.5
2365.5
2163
2161.5
2161.5
2150.5
2069.5
2069.5
2063
1373
1176
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1: /cgn2 6/ptodata/1/pubpaa/USO7 PUBCOMB.pep:*

2: /cgn2 6/ptodata/1/pubpaa/USO6 NEW PUB.pep:*

3: /cgn2 6/ptodata/1/pubpaa/USO6 NEW PUB.pep:*

4: /cgn2 6/ptodata/1/pubpaa/USO6 NEW PUB.pep:*

5: /cgn2 6/ptodata/1/pubpaa/USO7 NEW PUB.pep:*

6: /cgn2 6/ptodata/1/pubpaa/USO8 PUBCOMB.pep:*

7: /cgn2 6/ptodata/1/pubpaa/USO8 PUBCOMB.pep:*

8: /cgn2 6/ptodata/1/pubpaa/USO8 PUBCOMB.pep:*

9: /cgn2 6/ptodata/1/pubpaa/USO8 PUBCOMB.pep:*

10: /cgn2 6/ptodata/1/pubpaa/USO9 PUBCOMB.pep:*

11: /cgn2 6/ptodata/1/pubpaa/USO9 NEW PUB.pep:*

12: /cgn2 6/ptodata/1/pubpaa/USO9 NEW PUB.pep:*

13: /cgn2 6/ptodata/1/pubpaa/USO0 PUBCOMB.pep:*

14: /cgn2 6/ptodata/1/pubpaa/USO0 PUBCOMB.pep:*

15: /cgn2 6/ptodata/1/pubpaa/USO0 PUBCOMB.pep:*

16: /cgn2 6/ptodata/1/pubpaa/USO0 NEW PUB.pep:*

17: /cgn2 6/ptodata/1/pubpaa/USO0 NEW PUB.pep:*

18: /cgn2 6/ptodata/1/pubpaa/USO0 NEW PUB.pep:*

19: /cgn2 6/ptodata/1/pubpaa/USO0 NEW PUB.pep:*

19: /cgn2 6/ptodata/1/pubpaa/USO0 NEW PUB.pep:*

10: /cgn2 6/ptodata/1/pubpaa/USO0 NEW PUB.pep:*

11: /cgn2 6/ptodata/1/pubpaa/USO0 NEW PUB.pep:*

12: /cgn2 6/ptodata/1/pubpaa/USO0 NEW PUB.pep:*
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Gapop 10.0 , Gapext 0.5
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Maximum Match 100%
Listing first 45 summaries
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                US-10-272-291-8

US-10-389-566-797

US-10-389-566-1113

US-10-44-543-26

US-10-425-114-43176

US-10-424-599-202586

US-10-284-668-8

US-10-272-991-7

US-10-284-668-6

US-10-284-668-6

US-10-284-668-6

US-10-284-668-6

US-10-425-114-58577

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          Sequence 6, Appli
Sequence 797, App
Sequence 1213, App
Sequence 1213, App
Sequence 26, Appl
Sequence 202586,
Sequence 202586,
Sequence 6, Appli
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Sequence 6, Appli
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Sequence 3852, A
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nce 19	equence 19	equence 20	equence 98	equence 16	equence 23	equence 18	eguence 75	equence 47	equence 20	equence 29	equence 69	equence 39	equence 18	equence 21	equence 52	equence 4	equence	equence 22	equence 51	equence	equence	equence	equence	equence	equence	equence	equence 20	Φ 4.	equence 53
œ	030, A	582,	ูเบ  -  -	J	66,	58,	6, A	7, A	16,	9, A	, 69	36,	App	6147,	03,	$\vdash$	$\vdash$	$\sigma$		Appli	-	Appli	-	$\vdash$	~	-ب	-	×	

## ALIGNMENTS

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LENGTH: 799 amino acids
TYPE: amino acid
TOPOLOGY: linear
MOLECULE TYPE: protein
SEQUENCE DESCRIPTION: SEQ ID NO: 6:
US-09-952-677-6
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        NAME: Haley, Jr., James F.
REGISTRATION NUMBER: 27,794
REBERENCE/DOCKET NUMBER: AGREVO-9
TELECOMMUNICATION INFORMATION:
TELEPHONE: (212) 596-9000
TELEPHONE: (212) 596-9090
INFORMATION FOR SEQ ID NO: 6:
SEQUENCE CHARACTERISTICS:
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ATTORNEY/AGENT INFORMATION:
                                                                 721 GVRDTVPPFDPFNHSGLGWTFDRAEAHKLIEALGHCLRTYRDYKESWRGLQERGMSQDFS 780
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  361 GVRKYYKAAGQDMEVNYFHAYIDGVDFVFIDAPLFRHRQEDIYGGSRQEIMKRMILFCKA
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         VEEAPNPKALSPPAAPAVQEDLWDFKKYIGFEEPVEAKDDGWAVADDAGSFEHHONHDSG
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                        GLRDTVPPPPDPFNHSGLGWTFDRAEAHKLIEALGHCLRTYRDFKESWRALQERGMSQDFS
                                                                                                                HFEREHHDKVRGWVGFSVRLAHRITAGADALLMPSRFEPCGLNQLYAMAYGTVPVVHAVG
                                                                                                                                                    HFEREHHDKVRGWVGFSVRLAHRITAGADALLMPSRFEPCGLNQLYAMAYGTVPVVHAVG
                                                                                                                                                                                                     LQRELGLQVRADVPLLGFIGRLDGQKGVEIIADAMPWIVSQDVQLVMLGTGRHDLESMLQ
                                                                                                                                                                                                                                  LQRELGLQVRADVPLLGFIGRLDGQXGVEIIADAMPWIVSQDVQLVMLGTGRHDLESMLR 660
                                                                                                                                                                                                                                                                                             EGGWGLHDIIRQNDWKTRGIVNGIDNMEWNPEVDAHLKSDGYTNRSLRTLDSGKRQCKEA
                                                                                                                                                                                                                                                                                                                                    EGGWGLHDIIRONDWKTRGIVNGIDNMEWNPEVDVHLKSDGYTNFSLGTLDSGKROCKEA
                                                                                                                                                                                                                                                                                                                                                                                     QGRGPVDEFPFTELPEHYLEHFRLYDPVGGEHANYFAAGLKMADQVVVVSPGYLWELKTV
                                                                                                                                                                                                                                                                                                                                                                                                                         QGRGPVDEFPFTELPEHYLEHFRLYDPVGGEHANYFAAGLKMADQVVVVSPGYLMELKTV
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      AVEVPWHVPCGGVPYGDGNLVFIANDWHTALLPVYLKAYYRDHGLMQYTRSIMVIHNIAH
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95.6%;
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Pred. No. 3.2e-312;
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CURRENT FILING DATE: 2002-10-17
PRIOR APPLICATION NUMBER: 60/329,525
PRIOR FILING DATE: 2001-10-01
NUMBER OF SEQ ID NOS: 8
SOFTWARE: PATENTIN Ver. 2.1
SEQ ID NO 8
LENGTH: 641
TYPE: PRT
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US-10-272-291-8
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publication No. US20030150023A1
GENERAL INFORMATION:
APPLICANT: ExSeed Genetics
TITLE OF INVENTION: Starch
FILE REFERENCE:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Best Loc
Matches
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         167 GDNDSGPLAGENVMNVIVVAAECSPWCKTGCLGDVVGALPKALARRGHRVMVVVPRYGDY
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  176 PTSIAEVVAPDSAATISISDKAPESVVPAEKPPPSSGSNFVVSASAPRLDIDSDVEPELK 235
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       116 QDAARPPSMNGTPVNGENKSTGGGGATKDSGLPAPARAPHPSTQNRVPVNGENKANVASP 175
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             493;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Similarity
                          LESMLRHFEREHHDKVRGWVGFSVRLAHRITAGADALLMPSRFEPCGLNQLYAMAYGTVP
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   KGAVIVEEAPNPKALSPPAA-PAVQEDLWDFKKYIGFEEPVEAKDDGWAVADDAGSFEHH
                                                                    ROCKAALORELGLEVRODVPLLGFIGRLDGOKGVDIIGDAMPWIAGODVQLVMLGTGRAD
                                                                                                                                                            WELKTVEGGWGLHDIIRSNDWKINGIVNGIDHQEWNPKVDVHLRSDGYTNYSLETLDAGK
                                                                                                                                                                                                     WELKTVEGGWGLHDIIRQNDWKTRGIVNGIDNWEWNPEVDVHLKSDGYTNFSLGTLDSGK
                                                                                                                                                                                                                                                                                             IHNIAHQGRGPVDEFPFTELPEHYLEHFRLYDPVGGEHANYFAAGLKMADQVVVVSPGYL
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US-10-39-566-797
; Sequence 797, Application US/10389566
; Publication No. US20040025202A1
; GENERAL INFORMATION:
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US-10-389-566-797
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TITLE OF INVENTION: Nucleic Acid Molecules Associated with Oil in Plants
FILE REFERENCE: 38-77(52900)D
CURRENT APPLICATION NUMBER: US/10/389,566
CURRENT FILING DATE: 2003-03-31
PRIOR APPLICATION NUMBER: US 60/365,301
PRIOR APPLICATION NUMBER: US 60/365,301
PRIOR APPLICATION NUMBER: US 60/391,786
PRIOR FILING DATE: 2002-06-25
PRIOR PRIOR DATE: 2002-06-25
PRIOR PRIOR FILING DATE: 2002-06-25
PRIOR FILING DATE: 2002-06-26
NUMBER OF SEQ ID NOS: 2459
SOFTWARE: Patentin version 3.2
SEQ ID NO 797

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473 MVIHNIAHQGRGPVDEFPFTELPEHYLEHFRLYDPVGGEHANYFAAGLKMADQVVVVSPG 532
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                                                                 RMILFCKAAVEVPWFAPCGGSIYGDGNLVFIANDWHTALLPVYLKAYYRDNGLMQYTRSV 367
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US-10-389-566-1213
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CURRENT FILING DATE: 2003-03-31
PRIOR APPLICATION NUMBER: US 60/365,301
PRIOR FILING DATE: 2002-03-15
PRIOR FILING DATE: 2002-03-15
PRIOR RILING DATE: 2002-06-25
PRIOR RILING DATE: 2002-06-25
PRIOR APPLICATION NUMBER: US 60/392,018
PRIOR FILING DATE: 2002-06-26
VUMBER OF SEQ ID NOS: 2459
SOFTWARE: Patentin version 3.2
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US-10-389-566-1213
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GENERAL INFORMATION:
APPLICANT: Monsanto Technology, LLC
APPLICANT: Laurie, Cathy C
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TITLE OF INVENTION: Nucleic Acid Molecules Associated with Oil in Plants
FILE REFERENCE: 38-77(52900)D
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TYPE: PRT
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                                                                                                        233 ELKKGAVIVEEAPNPKALSPPAAPAVQEDL#DFKKYIGFEEPVEAKDDGWAVADDAGSFE 292
                                                                                                                                                                             101 VSSPKYVKPAVAKONGEVVS---RATKSDAFVSKPK-----VDPSVPASKAEAD--- 146
                                                                                                                                                                                                                                               173 ASPPTSIAEVVAPDSAATISISDKAPESVVFAEKPPPSSGSNFVVSASAPRLDIDSDVEP 232
                                                                                                                                                                                                                                                                                                                                                                                          113 APRQDAARPPSMNGTPVNGENKSTGGGGATKDSGLPAPARAPHPSTQNRVPVNGENKANV 172
                                                                                                                                                                                                                                                                                                                                                                                                                                                                   57 AVVCSASAAGG-----EDGVAKAK-----TKSA----
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        55 GV--AARAAGKKDARVDDDAASARQPRARRGGAATKVAERRDPVKTLDRDAAEGGAPAPP 112
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          1 MSGATASSPAATLFLAGSSSSSPR-RRRSRVSGVWWHLYGGTGLRLH---WERRGLVRDG 56
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               1 MSSAVAS---AASFLALASASFGRSRRRARVSAPPFH--AGAG-RLHWPFWFFQRTARDG 54
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                                                                                                                                                                                                                                                                                                                            RGMSQDFSWEHAAKLYEDVLLKAKYQW 799
                                          -GNAQAVESKAALDKKED------VGVAEPLEAKADAGGDAGAVSSAD 187
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RESULT 5
US-10-044-543-26
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         APPLICANT: Singletary, George
APPLICANT: Zhou, Lan
TITLE OF INVENTION: No. US20030135883A1el Starch Synthase Polynucleotides
TITLE OF INVENTION: and Their Use in the Production of New Starches
FILE REPERENCE: 114D
CURRENT APPLICATION NUMBER: US/10/044,543
CURRENT FILING DATE: 2002-01-11
PRIOR APPLICATION NUMBER: 09/388,743
PRIOR FILING DATE: 1999-09-02
NUMBER OF SEQ ID NOS: 28
SOFTMARE: PastSEQ for Windows Version 3.0
SEQ ID NO 26
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Sequence 26, Application US/10044543 Publication No. US20030135883A1 GENERAL INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                 Query Match
Best Local
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     LENGTH: 801
TYPE: PRT
ORGANISM: Typha latifolia
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                773 RGMSQDFSWEHAAKLYEDVILKAKYQW 799
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        473 MVIHNIAHQGRGPVDEEPFTELPEHYLEHFRLYDPVGGEHANYFAAGLKMADQVVVVSPG 532
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             413 RMILECKAAVEVPWHVPCGGVPYGDGNLVFIANDWHTALLPVYLKAYYRDHGLMQYTRSI 472
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                                                                                                                                                         192 SI-SDKAPE----SVVPAEKPPPSSG------
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  668 RGMAQDISWDHAAELYEDVLVKAKYQW 694
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          608 VPVVHÁVGGLRDTVAPFDPFADTGLGWTFDRÁBÁNRMIDÁLGHCLNTYRNYKESWRGLQA 667
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   713 VPVVHAVGGVRDTVPPFDPFNHSGLGWTFDRAEAHKLIEALGHCLRTYRDYKESWRGLQE 772
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 533 YLWELKTVEGGWGLHDIIRQNDWKTRGIVNGIDNMEWNPEVDVHLKSDGYTNFSLGTLDS 592
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                368 LVIHNIAHQGRGPVDDFATMDLPEHYIDHFRLYDPVGGEHSNVFAAGLKMADRAVTVSHG 427
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220 SAPRLDIDSDVEPELKKGAVIVEEAPNPKALSPP--AAPAVQEDIMDFKKYIGFEBPVEA 277
                                                                                                                                                                                                                                                                          134 KSTGGGGATKDSG--LPAPARAPHPSTONRVPVNGENKANVASPPTSIAEVVAPDSAATI 191
                                                                                                                                                                                                                 21 RATGKSGSFEEGGEREGVGRAGVGDDALRATIDKSNE--ILAIHSNLLQQIAKRKNIVS 78
                                                                                                                                                                                                                                                                                                                                   h 50.6%; Score 2163; DB 14; Length 801; Similarity 60.7%; Pred. No. 1.7e-161; 26; Conservative 84; Mismatches 151; Indels 41
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                                                                                             ŚIRŚDVTKEENDSSŚYVEKENLEPŚŚGEQNGKYKSGAVPNNYSQLAQDDTSENPLVNSFG 138
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            PDLEEMLRRFESEHNDKVRGWVGFSVQLAHRITAGADVLLMPSRFEPCGLNQLYAMAYST
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                                                                                                                                                                                                                                                                                                                                      Indels 41;
                                                                                                                                                         ----- SNFVVSA-- 219
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US-10-425-114-43176
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APPLICANT: Liu, Jingdong
APPLICANT: Zhou, Yihua
APPLICANT: Screen, Steven E
APPLICANT: Tabaska, Jack E
APPLICANT: Tabaska, Jack E
APPLICANT: Cao, Yongwei
TITLE OF INVENTION: Nucleic Acid Molecules and Other Molecules Associated With
TITLE OF INVENTION: Plants and Uses Thereof for Plant Improvement
FILE REFERENCE: 38-21 (5313)8
FILE REFERENCE: 38-21 (5313)8
FILE REFERENCE: 38-21 (5313)8
FILE REFERENCE: 30-203-04-28
RUMBER OF SEQ ID NOS: 73128
SEQ ID NO 43176
LENGTH: 535
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Sequence 43176, Application US/10425114 Publication No. US20040034888A1 GENERAL INFORMATION:
                                                                                                                                                                                                                                               Query Match
                                                                                                                                                                                                                                                                                                                                   OTHER INFORMATION: Clone ID: 700741124_FLI.pep
                                                                                                                                                                                                                                                                                                                                                                                           ORGANISM: Glycine max
                                                                                                                                                                                                                                                                                                                                                                    FEATURE:
                                                                                                                                                                                                                 Local Similarity
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          869
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    496 KSDGYTNYSLDTLEMGKPVCKAALQREVGLPVRDNVPIIAFIGRLDHQKGVDLIAEAMPW
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              616 EPCGLNQLYAMMYGTIPVVHAVGGLRDTVTQFDPFNESGLGWTFDRAEAGKLIHALNNCL
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             338 AKRGHRYMVVVPRYGDYEEAYDVGVRKYYKAAGQDMEVNYFHAYIDGVDFVFIDAPLFRH 397
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         198 KLDSVHVKDDLNPGE--ENEVPLPLAGANVMNIIVVAAECAPWSKTGGLGDVAGALPKAL 255
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     278 KDDGWAVADDAGSFEHHQNHDSGPLAGENVMNVVVVAAECSPWCKTGGLGDVAGALPKAL 337
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                                                                                                          284 VADDAGSFEHHQNHDSGPLAGENVMNVVVVAAECSPWCKTGGLGDVAGALPKALAKRGHR 343
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          676 NTYWNYKDSWKGLQTRGMMQDLSWDNAAQQYEDVLVAAKYQW 717
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      344 VMVVVPRYGDYEEAYDVGVRKYYKAAGQDMEVNYFHAYIDGVDFVFIDAPLFRHRQEDIY 403
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                                                                     VANEGDNVE-SKGENPPPLAGANVMVILVAAECAPFVKTGGLGDVAGSLPKALARRGHR 79
                                                                                                                                                                                       Conservative
                                                                                                                                                                                   50.5%; Score 2161.5; DB 12; Length 535; 74.8%; Pred. No. 1.3e-161; ative 64; Mismatches 65; Indels 1;
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US-10-424-599-202586
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SEQ ID NO 202586
LENGTH: 771
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Sequence 202586, Application US/10424599 Publication No. US20040031072A1
                                                                                                                                                                                                                                                                                                           Query Match
Best Local
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              APPLICANT: Zhou Yihua
APPLICANT: Cao Yongwei
TITLE OF INVENTION: Soy Nucleic Acid Molecules and Other Molecules Associated With
TITLE OF INVENTION: Plants and Uses Thereof for Plant Improvement
FILE REFERENCE: 38-21(5322)8
CURRENT APPLICATION NUMBER: US/10/424,599
CURRENT FILING DATE: 2003-04-28
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                APPLICANT: La Rosa Thomas J
APPLICANT: Kovalic David K
                                                                                                                                                                                                                                                                                                                                                                                                                                                          NAME/KEY: unsure
LOCATION: (1)..(771)
OTHER INFORMATION: unsure at all Xaa locations
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       TYPE: PRT
ORGANISM: Glycine max
FEATURE:
                                                                                                                                                                                                                                                                                                                                                                                                         OTHER INFORMATION: Clone ID: PAT_MRT3847_24960C.1.pep
                                                                                                                                                                                                                                                                                                                                                                                                                                       FEATURE:
                                                                                                                                                                                                                                                                                                           Local Similarity
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                                                                                                                           344 VMVVVERYGDYSEAYDVGVRKYYKAAGQDMEVNYFHAYIDGVDFVFIDAFLFRHRQEDIY 403
                                                                                                                                                                                                                           284 VADDAGSFEHHQNHDSGPLAGENVMNVVVVAAECSPWCKTGGLGDVAGALPKALAKRGHR 343
                                                                                                                                                                                                                                                                                  386;
                                                                                                                                                                               257 VANEGDNVE-SKGENPPPLAGANVMVILVAAECAPFVKTGGLGDVAGSLPKALARRGHR 315
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GGSRQEIMKRMILFCKAAVEVFWHVPCGGVFYGDGNLVEIANDWHTALLFVYLKAYYRDH 463
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                                                                               VMVVVPRYSHYADAQDIGVWKRYKVDGQDMEVTYFHSYIDGVDFVFIDSPNFRHLQDNIY 375
                                                                                                                                                                                                                                                                                  Conservative
                                                                                                                                                                                                                                                                             50.5%; Score 2161.5; DB 12 74.8%; Pred. No. 2.2e-161; tive 64; Mismatches 65;
                                                                                                                                                                                                                                                                                                                                 DB 12; Length 771;
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US-10-284-668-8
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                                              NAME: Haley Jr., James F.
REGISTRATION NUMBER: 27,794
REFERBNCE/DOCKET NUMBER: Agreve-4
TELECOMMUNICATION INFORMATION:
TELEPHONE: 212-596-9000
TELEPHONE: 212-596-9090
INFORMATION FOR SEQ ID NO: 8:
SEQUENCE CHARACTERISTICS:
                                                                                                                                                                                                                                                 PRIOR APPLICATION DATA:
APPLICATION NUMBER: US/08/836,567
FILING DATE: 24-UL-1997
APPLICATION NUMBER: PCT/EP95/04415
FILING DATE: 09-NOV-1995
APPLICATION NUMBER: DE P 44 41 408.0
FILING DATE: 10-NOV-1994
ATTORNEY/AGENT INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: PatentIn Release #1.0, Version #1.30
CURRENT APPLICATION DATA:
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CORRESPONDENCE ADDRESS:
ADDRESSEE: FISH & NEAVE
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TITLE OF INVENTION: DNA MOLECULES THAT CODE FOR ENZYMES
INVOLVED IN STARCH SYNTHESIS VECTORS BACTERIA TRANSGENIC
PLANT CELLS AND PLANTS CONTAINING SAID MOLECULES
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MEDIUM TYPE: Floppy disk
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Springer, Franziska
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                                                                                                                                                                                                                                                                                                                                                                                                                                                             APPLICATION NUMBER: US/10/284,668 FILING DATE: 29-Oct-2002 CLASSIFICATION: <Unknown>
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 STATE: New York
COUNTRY: USA
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        LENGTH: 767 amino acids TYPE: amino acid
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; TOPOLOGY: linear; MOLECULE TYPE: protein; SEQUENCE DESCRIPTION: SEQ ID NO: US-10-284-668-8
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763 AKYOW 767
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                                    AKYOW 799
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        AECSPWCKTGGLGDVAGALPKALAKRGHRVMVVVPRYGDYEEAYDVGVRKYYKAAGQDME 374
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                                                                                                                                                                                                                                                                                          LLGFIGRLDGQKGVEIIADAMPWIVSQDVQLVMLGTGRHDLESMLRHFEREHHDKVRGWV
                                                                                                                                                                                                                                                                                                                                      WKLQGIVNGIDTKEWNPELDVHLQSDGYMNYSLDTLQTGKPQCKAALQKELGLPVRDDVP
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 VNYFHAYIDGVDFVFIDAPLFRHRQEDIYGGSRQEIMKRMILFCKAAVEVPWHVPCGGVP 434
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            SECAPWSKTGGLGDVÄGÄLPKALARRGHRVMVVAPRYDNYPEPQDSGVRKIYKVDGQDVE 342
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                                                                                                                                                                                                   GFSVRLAHRITAGADALLMPSRFBPCGLNQLYAMAYGTVPVVHAVGGVRDTVPPPDPFNH
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                                                                                SCIGWTFSRAEASQLIHALGNCLLTYREYKKSWEGIQTRCMTQDLSWDNAAQNYEEVLIA
                                                                                                                     SGLGWTFDRAEAHKLIEALGHCLRTYRDYKESWRGLQERGMSQDFSWEHAAKLYEDVLLK 794
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RESULT 9 US-10-272-291-7

Sequence 7, Application US/10272291
Publication No. US20030150023A1
GENERAL INFORMATION:
APPLICANT: Exseed Genetics
TITLE OF INVENTION: Starch

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; ORGANISM: Zea mays
; PEATURE:
OTHER INFORMATION: Starch Synthase IIb-2 (N-terminally truncated
; OTHER INFORMATION: SSIIb)
US-10-272-291-7
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; Sequence 6, Application US/10044543
; Publication No. US20030135883A1
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GENERAL INFORMATION:

APPLICANT: Singletary, George
TITLE OF INVENTION: No. US20030135883A1el Starch Synthase Polynucleot
TITLE OF INVENTION: No. US20030135883A1el Starch Synthase Polynucleot
TITLE OF INVENTION: No. US2003135883A1el Starch Synthase Production of New Starches
FILE REPERRICE: 1144D
CURRENT FILING DATE: 2002-01-11
PRIOR APPLICATION NUMBER: 09/388,743
PRIOR FILING DATE: 1999-09-02
NUMBER OF SEQ ID NOS: 28
SOFTWARE: FastSEQ for Windows Version 3.0
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CURRENT FILING NUMBER: US/10/272,291
CURRENT FILING DATE: 2002-10-17
PRIOR APPLICATION NUMBER: 60/329,525
PRIOR FILING DATE: 2001-10-01
NUMBER OF SEQ ID NOS: 8
SOFTWARE: Patentin Ver. 2.1
SEQ ID NO 7
SEQ ID NO 7
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Best Local
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                368 AAGQDMEVNYFHAYIDGVDFVFIDAPLFRHRQEDIYGGSRQEIMKRMILFCKAAVEVPWH 427
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RESULT 11
US-10-284-668-6
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; LENGTH: 690
; TYPE: PRT
; ORGANISM: Curcuma z
                                                                                  Sequence 6, Application US/10284668 Publication No. US20030106100A1 GENERAL INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Query Match
Best Local
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APPLICANT: Kossmann, Jens
Springer, Franziska
Springer, Franziska
Abel, Gernot
TITLE OF INVENTION: DNA MOLECULES THAT CODE FOR ENZYMES
INVOLVED IN STARCH SYNTHESIS VECTORS BACTERIA TRANSGENIC
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Similarity 56.0%;
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                                                                                                                                                                                                                                    QW 799
                                                                                                                                                                                                                                                                      GWTFDRAEAHRMIVALGHCLNTYRNYKESWVGLQKRGMMQDLSWESAAEHYEKVLVAAKY
                                                                                                                                                                                                                                                                                                                                   VXMAHRITAGADALLMPSRFEECGLNQLHAMMYGTIPVVHAVGGLRDTVQQFDEFNETGL
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                                                                                                                                                                                                     Ó₩ 690
                                                                                                                                                                                                                                                                                                  GWTFDRAEAHKLIEALGHCLRTYRDYKESWRGLQERGMSQDFSWEHAAKLYEDVLLKAKY 797
                                                                                                                                                                                                                                                                                                                                                                                                     FIGRLDHQKGIDLÍAEAMHWLVGQDLQIIMLGTGRPDLEDMLRRFEREHRGKVRGWVGFS
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Pred. No. 1.1e-153;
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COMPUTER: IEM PC COMPLETED:
COMPUTER: IEM PC COMPLETED:
SOFTWARE: PATENTIN Release #1.0, Version #1.30
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/10/284,668
FILING DATE: 29-Oct-2002
CLASSIFICATION NUMBER: US/08/836,567
FILING DATE: 24-OUL-1997
APPLICATION NUMBER: US/08/836,567
FILING DATE: 09-NOV-1995
APPLICATION NUMBER: DE P 44 41 408.0
FILING DATE: 10-NOV-1995
APPLICATION NUMBER: DE P 44 41 408.0
FILING DATE: 10-NOV-1994
APPLICATION NUMBER: DF 7,794
REPERENCE/DOCKET NUMBER: Agrevo-4
REGISTRATION INFORMATION:
TELEPHONE: 212-596-9000
INFORMATION FOR SEQ ID NO: 6:
SEQUENCE CHARACTERISTICS:
LENGTH: 568 amino-acids
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           ZIP: 10020
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     LENGTH: 558 amino acids
TYPE: amino acid
TOPOLOGY: linear
MOLECULE TYPE: protein
SEQUENCE DESCRIPTION: SEQ ID NO: 6:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     NUMBER OF SEQUENCES: 17
CORRESPONDENCE ADDRESS:
ADDRESSEE: FISH & NEAVE
                                                                                                                                                                                                                                                                                                                                                                                                                                                                       421 AVEVPWHYPCGGYPYGDGNLYFIANDWHTALLFYYLKAYYRDHGLMQYTRSIMVIHNIAH 480
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            301 PLAGENVANVVVVAAECSPWCKTGGLGDVAGALPKALAKRGHRVMVVVPRYGDYEEAYDV 360
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CITY: New York
STATE: New York
                             HFEREHHDKVRGWVGFSVRLAHRITAGADALLMPSRFEPCGLNQLYAMAYGTVPVVHAVG
                                                                                                                                       LQRELGLQVRADVPLLGFIGRLDGQKGVEIIADAMFWIVSQDVQLVMLGTGRHDLESMLR 660
                                                                                                                                                                                                                                                                                                                                                                        QGRGPVDEFPFTELPEHYLEHFRLYDPVGGEHANYFAAGLKMADQVVVVSPGYLWELKTV 540
                                                                                                                                                                                                                                                                    EGGWGLHDIIRQNDWKTRGIVNGIDNMEWNPEVDVHLKSDGYTNFSLGTLDSGKRQCKEA 600
                                                                                                                                                                                                                                                                                                                                                                                                                                      ALEVPWHVPCGGVCYGDGNLVFIANDWHTALLPVYLKAYYRDNGIMNYTRSVLVIHNIAH
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           GVRKIYKVDGQDVEVTYFQAFIDGVDFVFID3HMFRHIGNNIYGGNRVDILKRMVLFCKA 179
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   GVRKYYKAAGQDMEVNYFHAYIDGVDFVFIDAPLFRHRQEDIYGGSRQEIMKRMILFCKA 420
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           PLAGTNVMNIILVASECAPWSKTGGLGDVAGALPKALARRGHRVMVVAPRYDNYPEPQDS 119
QFECQHNDKIRGWVGFSVKTSHRITAGADILLMPSRFEALRLNQLYAMKYGTIPVVHAVG
                                                                                                       <u>LQKELGLPVRDDVPLIGFIGRLDPQKGVDLIAEASAWMMGQDVQLVMLGTGRRDLEQMLR</u>
                                                                                                                                                                                                                 QGGWGLHQIINENDWKLQGIVNGIDTKEWNPELDVHLQSDGYMNYSLDTLQTGKPQCKAA
                                                                                                                                                                                                                                                                                                                         QGRGPLEDFSYVDLPPHYMDPFKLYDPVGGEHFNIFAAGLKTADRVVTVSHGYSWELKTS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       48.2%; Score 2059; DB 14; 73.7%; Pred. No. 1.7e-153;
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US-10-425-114-38552
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Publication No. US20040034888A1
GENERAL INFORMATION:
APPLICANT: Liu, Jingdong
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Query Match
Best Local Similarity
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             APPLICANT: Zhou, Yihua
APPLICANT: Kovalic, David K.
APPLICANT: Screen, Steven E
APPLICANT: Screen, Steven E
APPLICANT: Tabaska, Jack E
APPLICANT: Cao, Yongwei
TITLE OF INVENTION: Nucleic Acid Molecules and Other Molecules Associated With
TITLE OF INVENTION: Plants and Uses Thereof for Plant Improvement
FILE REFERENCE: 38-21 (53313) B
CURRENT APPLICATION NUMBER: US/10/425,114
CURRENT FILING DATE: 2003-04-28
NUMBER OF SEQ ID NOS: 73128
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Matches 348;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 ORGANISM: Zea mays
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ENGTH: 440
  421
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                                                   780 SWEHAAKLYEDVLIKAKYOW 799
                                                                                                                                                                                                                                                                                                                                                 600 ALQREIGLQVRADVPLLGFIGRLDGQKGVEIIADAMPWIVSQDVQLVMLGTGRHDLESML
                                                                                                                                                                                                                                                                                                                                                                                                     181 SEGGWGLHDIINQNDWKLQGIVNGIDMSEWNPAVDVHLHSDDYTNYTFETLDTGKRQCKA 240
                                                                                                                                                                                                                                                                                                                                                                                                                                                      540 VEGGWGLHDIIRQNDWKTRGIVNGIDNMEWNÞEVDVHLKSDGYTNFSLGTLDSGKRQCKE 599
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       121 HOGRGPVDDFVNFDLPEHYIDHFKLYDNIGGDHSNVFAAGLKTADRVVTVSNGYMWELKT 180
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     480 HOGRGPYDEFPFTELPEHYLEHFRLYDPYGGEHANYFAAGLKMADQVVVVVSPGYLWELKT
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         61 ÁAVEVPWYAPCGGTVYGDGNÍVFIANDWHTALLPVYLKÁYYRDNGLMQYARSVLVIHNIA 120
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SWDHAAVLYEDVLVKAKYQW 440
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                                                                                                    GGLRDTVAPFDPFNDTGLGWTFDRAEANRMIDALSHCLTTYRNYKESWRGLQARGMAQDL 420
                                                                                                                             GGVRDTVPPFDFFNHSGLGWTFDRAEAHKLIEALGHCLRTYRDYKESWRGLQERGMSQDF 779
                                                                                                                                                                                                    RRFESEHSDKVRAWVGFSVPLAHRITAGADILLMPSRFEPCGLNQLYAMAYGTVPVVHAV 360
                                                                                                                                                                                                                                                  RHFEREHHDKVRGWVGFSVRLAHRITAGADALLMPSRFEPCGLNQLYAMAYGTVPVVHAV 719
                                                                                                                                                                                                                                                                                                   ALQRQLGLQVRDDVPLIGFIGRLDHQXGVDIIADAIHWIAGQDVQLVMLGTGRADLEDML 300
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79.1%; Pred. No. 1e-143;
7ative 40; Mismatches 52; Indels
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US-10-425-114-58577

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                                                                                                                                                                                                                                                                                                                                                                                                                    RESULT 14
US-10-284-668-10
; Sequence 10, Application US/102
; Publication No. US20030106100A1
; GENERAL INFORMATION:
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APPLICANT: Zhou, Yihua
APPLICANT: Shou, Yihua
APPLICANT: Screen, Steven E
APPLICANT: Screen, Steven E
APPLICANT: Tabaska, Jack E
APPLICANT: Tabaska, Jack E
APPLICANT: Cao, Yongwei
TITLE OF INVENTION: Nucleic Acid Molecules and Other Molecules Associated With
TITLE OF INVENTION: Plants and Uses Thereof for Plant Improvement
FILE REFERENCE: 38-21(53313)B
CURRENT APPLICATION NUMBER: US/10/425,114
CURRENT APPLICATION STEEL 2003-04-28
NUMBER OF SEQ ID NOS: 73128
SEQ ID NO 58577
LENGTH: 341
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Sequence 58577, Application US/10425114
Publication No. US20040034888A1
GENERAL INFORMATION:
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ORGANISM: Zea mays
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        FEATURE:
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COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
                                                                                                                                                                                  CORRESPONDENCE ADDRESS:
ADDRESSEE: FISH & NEAVE
                                                                                                                                                                                                                                                              TITLE OF INVENTION: DNA MOLECULES THAT CODE FOR ENZYMES
INVOLVED IN STARCH SYNTHESIS VECTORS BACTERIA TRANSGENIC
PLANT CELLS AND PLANTS CONTAINING SAID MOLECULES
                                                                                                                                                                                                                                                                                                                                        APPLICANT: Kossmann, Jens
Springer, Franziska
Abel, Gernot
                                                                                                                                                                                                                                  NUMBER OF SEQUENCES:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  579 SDGYTNFSLGTLDSGKRQCKEALQRELGLQVRADVPLLGFIGELDGQKGVEIIADAMPWI 638
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       301 TYRNYWSSWEGIORRGMMODLSWDNAAKLYEEVILAAKYOW 341
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                181 AGODVOLIMIGTGRODIEDTIRRIESOHYDRVRGWVGFSVRIAHRMTAGADILIMPSRFE
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            519 GLKMADQVVVVSPGYLWELKTVEGGWGLHDIIRQNDWKTRGIVNGIDNMEWNPEVDVHLK 578
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  459 YYRDHGIMQYTRSIMVIHNIAHQGRGPVDEFPFTELPEHYLEHFRLYDPVGGEHANYFAA 518
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            61 GIRAADRILITVSHGYAWELKTPDGGWGLHSIINENDWKFQGIVNGIDTADWNPRHDVHLQ
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                                                                            CITY: New York
STATE: New York
COUNTRY: USA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         SDGYTNYSLETVQTGKAQCKEALQKELGLPVRGDVPVIAFIGRLDHQKGVDLIAEAMPWI 180
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         TYRDYKESWRGLQERGMSQDFSWEHAAKLYEDVLLKAKYQW 799
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               PCGLNQLYAMMYGTVPVVHAVGGLRDTVQHYNPYEEVGVGWTFEKAEANRMIDALGHCLN 300
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             PCGLNQLYAMAYGTVPVVHAVGGVRDTVPPFDPFNHSGLGWTFDRAEAHKLIEALGHCLR 758
                                                     ZIP: 10020
                                                                                                                                                        STREET: 1251 Avenue of the Americas
                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Application US/10284668
                                                                                                        York
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     51; Mismatches 52;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          0,
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Query Match 27.5%; Score 1176; DB 14; Length 641; Best Local Similarity 45.2%; Pred. No. 8.3e-84; Matches 250; Conservative 72; Mismatches 181; Indels 50
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INFORMATION FOR SEQ ID NO: 10:
SEQUENCE CHARACTERISTICS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             APPLICATION NUMBER: PCT/EP95/04415
FILING DATE: 09-NOV-1995
APPLICATION NUMBER: DF 44 41 408.0
FILING DATE: 10-NOV-1994
ATTORNEY/AGENT INFORMATION:
NAME: Haley Jr., James F.
REGISTRATION NUMBER: 27,794
REGISTRATION INFORMATION:
TELEPHONE: 212-596-9000
TELEPHONE: 212-596-9000
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      LENGTH: 641 amino acids
TYPE; amino acid
TOPOLOGY: linear
MOLECULE TYPE: protein
SEQUENCE DESCRIPTION: SEQ ID NO: 10:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          PRIOR APPLICATION DATA:
APPLICATION NUMBER: US/08/836,567
FILING DATE: 24-JUL-1997
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: PATENTIN RELEASE #1.0, Version #1.30
CURRENT APPLICATION DATA:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       331 GALÞKALAKRGHRVMVVVPRY------GDYEEAYDVGVRKYYKAAGQDMEVNYFHAYID 383
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               283 AVADDAGSFEHHQ--NHDSGPLAGEN------VMNVVVVAAECSPWCKTGGLGDVA 330
                                                                                                                                                                                                                                                                            671 RGWVGFSVRLAHRITAGADALLMPSRFEPCGLNQLYAMAYGTVPVVHAVGGVRDTVPPFD 730
                                                                                                                                                                                                                                                                                                                                                                                                       611 ADVPLLGFIGRLDGOKGVEIIADAMPWIVSQDVQLVMLGTGRHDLESMLRHFEREHHDKV 670
                                                                                                                                                                                                                                                                                                                                                                                                                                                                    390 SSRQSVLNGITNGIDVNDWNPSTDEHIAS----HYSINDL-SGKVQCKTDLQKELGLPIR 444
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 551 RONDWKTRGIVNGIDNMEWNPEVDVHLKSDGYTNFSLGTLDSGKRQCKEALQRELGLQVR 610
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  330 YGAVEWIFPTWARAHALDTGETVNVLKGAIAVADRILTVSQGYSWEITTPEGGYGLHELL
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            499 LEHFRLYDPV-----GGEHANYFAAGLKMADQVVVVSPGYLWELKTVEGGWGLHDII 550
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             270 KCLFLANDWHAALVELLLAAKYRPYGVYKDARSIVAIHNIAHQGVEFAVTYNNLGLPPQW 329
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                439 NLVFIANDWHTALLPVYLKAYYRDHGLMQYTRSIMVIHNIAHQGRGPVDEFPFTELPEHY 498
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              384 GVDFVFIDAPLFRH---RQEDIYG--GSRQEIMKRMILFCKAAVEVPWHVPCGGVPYGDG 438
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           154 GSLPMALAARGHRVMVVSPRYLNGGPSDEKYANAVDLDVRATVHCFGDAQEVAFYHEYRA 213
                           787 LYEDVLLKAKYQW 799
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     94 SVAGDATMVÉSHDIVANDRODLSEDTEEMEETPIKLTFNIIFVTAEAAPYSKTGGLGDVC 153
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    GVDWVFVDHSSYCRPGTPYGDIYGAFGDNQ---FRFTLLSHAACEAPLVLPLGGFTYGE- 269
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     APPLICATION NUMBER: US/10/284,668 FILING DATE: 29-Oct-2002 CLASSIFICATION: <Unknown>
                                                                                           PYAQEGIGEGIGWTFSPLTSEKLLDTLKLAIGTYTEHKSSWEGLMRRGMGRDYSWENAAI 624
                                                                                                                                                                                                                   RAWVGFNVPVSHRITAGCDILLMPSRFEPCGLNQLYAMRYGTIPIVHSTGGLRDTVXDFN 564
                                                                                                                                                                                                                                                                                                                                             PDCPLIGFIGRLDYQKGVDIILSAIPELMQNDVQVVMLGSGEKQYEDWMRHTENLFKDKF
                                                                                                                                                  PFNHSGL----GWTFDRAEAHKLIEALGHCLRTYRDYKESWRGLQERGMSQDFSWEHAAK 786
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   50;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         TOPOLOGY: linear

MOLECULE TYPE: protein

SEQUENCE DESCRIPTION: SEQ ID NO: 2:
US-09-952-677-2
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 RESULT 15
US-09-952-677-2
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PRIOR APPLICATION NUMBER: US/09/952,677

FILING DATE: 14.569,2001

PRIOR APPLICATION NUMBER: 09/196,390

FILING DATE: 19-No. US20020138876A1-1998

APPLICATION NUMBER: DE 196 21.528.9

FILING DATE: 19-No.Y-1996

APPLICATION NUMBER: DE 196 36.917.7

FILING DATE: 11-SEP-1996

APPLICATION NUMBER: DE 196 36.917.7

FILING DATE: 28-NaY-1997

APPLICATION NUMBER: PCT/EP97/02793

FILING DATE: 28-NaY-1997

ATTORNEY/AGENT INFORMATION:

REGISTRATION NUMBER: AGREVO-9

REGISTRATION NUMBER: AGREVO-9

TELECOMMUNICATION INFORMATION:

TELECOMMUNICATION INFORMATION:

TELECOMMUNICATION INFORMATION:

TELECOMMUNICATION INFORMATION:

TELEFAX: (212) 596-9000

TELEFAX: (212) 596-9000

INFORMATION FOR SEQ ID NO: 2:

SEQUENCE CHARACTERISTICS:

LENGTH: 671 amino acids

TYPE: amino acids

TOPOLOGY- 11 Near
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                                                                                                                                                                                                                                                                                                                                                                               Matches 237;
                                                                                                                                                                                                                                                                                                                                                                                                          Query Match
Best Local
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       CORRESPONDENCE ADDRESS:
ADDRESSEE: James F. Haley, Jr., 2/o
STREET: 1251 Avenue of the Americas
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Frohberg, Claus
Kossmann, Jens
TITLE OF INVENTION: NUCLEIC ACID MOLECULES ENCODING ENZYMES
FROM WHEAT WHICH ARE INVOLVED IN STARCH
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        COMPUTER READABLE FORM:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             NUMBER OF SEQUENCES:
174 AACEAPLILELGGYIYGQ-NCMEVVNDWHASLVPVLLAAKYRPYGVYRDSRSTLVIHNLA
                                                   420 AAVEVPWHVPCGGVPYGDGNLVFIANDWHTALLPVYLKAYYRDHGLMQYTRSIMVIHNIA 479
                                                                                                                       115 HIKIPCFGGSHEVTFFHEYRDNVDWVFVDHPSY-HRPGSLYGDNFGAFGDNQFRYTLLCY 173
                                                                                                                                                                                                                                                                                                           309 NVVVVAAECSPWCKTGGLGDVAGALPKALAKRGHRVMVVVPRY----GDYBBAYDVGVRK 364
                                                                                                                                                                                    365 YYK--AAGQDMEVNYFHAYIDGVDFVFIDAFLFRHRQEDIYG---GSRQEIMKRMILFCK 419
                                                                                                                                                                                                                                                     55 SIVFVTGEAAPYAKSGGLGDVCGSLPIALAARGHRVMVVMPRYLNGSSDKNYAKALYTAK 114
                                                                                                                                                                                                                                                                                                                                                                                                              Similarity
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC Compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patentin Release #1.0, Version #1.30 (EPO)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  COUNTRY: United States of America
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    STATE: New York
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                                                                                                                                                                                                                                                                                                                                                                        26.6%; Score 1138.5; DB 9; Length ilarity 47.8%; Pred. No. 83-81; Conservative 71; Mismatches 161; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          10020
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Walter, Lennart
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            SYNTHESIS
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US-10-284-668-10

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Gaps

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Search completed: March 17, 2004, 19:37:08 Job time: 47 secs
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                                                                                         468 TVPVVHGTGGLRDTVETFNPFGAKGEEGTGWAFSPLTVDKMLWALRTAMSTFREHKDSWE 527
                                                                                                              712 TVPVVHAVGGVRDTVPPFDPF---NHSGLGWTFDRAEAHKLIEALGHCLRTYRDYKESWR 768
                                                                                                                                      233 HQGVEPASTYPDLGLPPEWYGALEWVFPEWARRHALDKGEAVNFLKGAVVTADRIVTVSQ 292
                                                                                                                                                                                                                                                                                                     480 HOGRGPVDEFPFTELPEHYL-----EHFRLYDPVGGEHANYFAAGLKWADQVVVVSP 531
                                                                 769 GLQERGMSQDFSWEHA 784
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